

SEQUENCE LISTING

<110> Merck & Co., Inc.
Sano, Hideki
Tan, Carina P.
Howard, Andrew D.

<120> RHESUS MONKEY BOMBESIN RECEPTOR
SUBTYPE-3 (BRS-3), NUCLEOTIDES ENCODING SAME, AND USES
THEREOF

<130> 21198-PCT

<150> 60/463,776

<151> 2003-04-18

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1197

<212> DNA

<213> Macaca mulatta

<400> 1

```

atgggtcaaaa ggcagcctca ctcacctaata cagactttaaa tttcaatcac aaatgacaca 60
gaatcaagct ctgtgggtttc taacgataac acaaataaag gacggagcgg ggacaactct 120
ccaggaatag aagcattgtg tgccatctat attacttatg ctgtgatcat ttcagtgggc 180
atccttggaa atgctattct catcaaagtc tttttcaaga ccaaataccat gcaaacagtt 240
ccaaatattt tcatcaccag cctggctttt ggagatcttt tactttctgct aacttgtgtg 300
ccagtggatg caaccacta ccttgcagaa ggatggctgt tcggaagaat tggttgtaag 360
gtgctctctt tcatccggct cacttctgtt ggtgtgtcag tgttcaogtt aacaattctc 420
agcgtgaca gatacaaggc agtttgtgaag ccacttgagc gacagccctc caatgccatc 480
ctgaagactt gtataaaaagc tggctgcgtc tggatcgtgt ctatgatatt tgctctacct 540
gaggctatat tttcaaatgt atattctttt cgagatccca acaaaaatgt gacatttgaa 600
tcgtgtacct cttatcctgt ctctaagaag ctcttgcaag aaatacattc tctgctgtgc 660
ttcttagtgt tctacattat tccactctct attatctctg tctattatto tttgattgct 720
aggacccttt ataaaagcac cctgaacata cctactgagg aacaaggcca tgcccgtgaa 780
cagattgaat cccggaagag aattgccaga acggtattgg tggttggtggc tctgtttgcc 840
ctctgtgtgt tgcctaatca cctcctgtac ctctaccatt cattcacttc tcaaacctat 900
gtagaccctt ctgccatgca tttcattttt accattttct ctcggtttct ggctttcagc 960
aattcttgcg taaacccctt tgctctctac tggctgagca aaaccttcca gaagcatttt 1020
aaagctcagt tgttctgttg caaggcagag cagcctgagc ctctgtgtgc tgacacctct 1080
cttaccaccc tggctgtgat ggggaagggtc ccgggcaactg ggaacatgca gatgtctgaa 1140
attagtgtga cctcgtttcc tgggtgtagt gtgaagcagg cagaggatag agtctag 1197

```

<210> 2

<211> 398

<212> PRT

<213> Macacca mulatta

<400> 2

```

Met Ala Gln Arg Gln Pro His Ser Pro Asn Gln Thr Leu Ile Ser Ile
 1           5           10
Thr Asn Asp Thr Glu Ser Ser Ser Val Val Ser Asn Asp Asn Thr Asn
          20          25          30
Lys Gly Arg Ser Gly Asp Asn Ser Pro Gly Ile Glu Ala Leu Cys Ala
          35          40          45
Ile Tyr Ile Thr Tyr Ala Val Ile Ile Ser Val Gly Ile Leu Gly Asn
          50          55          60
Ala Ile Leu Ile Lys Val Phe Phe Lys Thr Lys Ser Met Gln Thr Val
65          70          75          80

```

Pro Asn Ile Phe Ile Thr Ser Leu Ala Phe Gly Asp Leu Leu Leu Leu
 85 90 95
 Leu Thr Cys Val Pro Val Asp Ala Thr His Tyr Leu Ala Glu Gly Trp
 100 105 110
 Leu Phe Gly Arg Ile Gly Cys Lys Val Leu Ser Phe Ile Arg Leu Thr
 115 120 125
 Ser Val Gly Val Ser Val Phe Thr Leu Thr Ile Leu Ser Ala Asp Arg
 130 135 140
 Tyr Lys Ala Val Val Lys Pro Leu Glu Arg Gln Pro Ser Asn Ala Ile
 145 150 155 160
 Leu Lys Thr Cys Ile Lys Ala Gly Cys Val Trp Ile Val Ser Met Ile
 165 170 175
 Phe Ala Leu Pro Glu Ala Ile Phe Ser Asn Val Tyr Ser Phe Arg Asp
 180 185 190
 Pro Asn Lys Asn Val Thr Phe Glu Ser Cys Thr Ser Tyr Pro Val Ser
 195 200 205
 Lys Lys Leu Leu Gln Glu Ile His Ser Leu Leu Cys Phe Leu Val Phe
 210 215 220
 Tyr Ile Ile Pro Leu Ser Ile Ile Ser Val Tyr Tyr Ser Leu Ile Ala
 225 230 235 240
 Arg Thr Leu Tyr Lys Ser Thr Leu Asn Ile Pro Thr Glu Glu Gln Gly
 245 250 255
 His Ala Arg Lys Gln Ile Glu Ser Arg Lys Arg Ile Ala Arg Thr Val
 260 265 270
 Leu Val Leu Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Asn His Leu
 275 280 285
 Leu Tyr Leu Tyr His Ser Phe Thr Ser Gln Thr Tyr Val Asp Pro Ser
 290 295 300
 Ala Met His Phe Ile Phe Thr Ile Phe Ser Arg Val Leu Ala Phe Ser
 305 310 315 320
 Asn Ser Cys Val Asn Pro Phe Ala Leu Tyr Trp Leu Ser Lys Thr Phe
 325 330 335
 Gln Lys His Phe Lys Ala Gln Leu Phe Cys Cys Lys Ala Glu Gln Pro
 340 345 350
 Glu Pro Pro Val Ala Asp Thr Ser Leu Thr Thr Leu Ala Val Met Gly
 355 360 365
 Arg Val Pro Gly Thr Gly Asn Met Gln Met Ser Glu Ile Ser Val Thr
 370 375 380
 Ser Phe Pro Gly Cys Ser Val Lys Gln Ala Glu Asp Arg Val
 385 390 395

<210> 3
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 3
 ttggacgtga caatcactgt atttgaactg aga

33

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 4
 tgttttctcct cccagcatgt gatatccg

27

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 5
gctctcttttc atccggctc 19

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
ctgccttgta tctgtcagcg 20

<210> 7
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
catgcccgta agcagggtt 18

<210> 8
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
cagcagaggg caaacagag 19

<210> 9
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
atgggatccg ccaccatggc tcaaaggcag cctcactcac ct 42

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 10

atgctcgagt ggaaagctag actctatcct ctgcctgc 38
<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 11
gaaagagagc accttacaac caatt 25
<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 12
ccagtggatg caacccta 20
<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 13
ttccgaacag ccataccttct gcaag 25
<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 14
gcaagcagga gtagacgag tct 23
<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 15
aactaagtca cagtccgcct agaag 25
<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer

<400> 16
cccttccatc gtccaccgca aat

23

<210> 17
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 17
atggctcaaa ggcagcctca ctcacctaata cagacttta tttcaatcac aaatgacaca 60
gaatcatcaa gctctgtggt ttctaacgat aacacaaata aaggatggag cggggacaac 120
tctccaggaa tagaagcatt gtgtgccatc tatattactt atgctgtgat catttcagtg 180
ggcatccttg gaaatgctat tctcatcaaa gtctttttca agaccaaatc catgcaaaca 240
gttccaaata ttttcatcac cagcctggct tttggagatc ttttacttct gctaacttgt 300
gtgccagtgg atgcaactca ctaccttgca gaaggatggc tgttcggaag aattgggtgt 360
aagggtgctc ctttcatccg gctcacttct gttaggtgtg cagtgttcac attaacaatt 420
ctcagcgtcg acagatacaa ggcagttgtg aagccacttg agcgacagcc ctccaatgcc 480
atcctgaaga cttgtgtaaa agctggctcg gtctggatcg tgtctatgat atttgctcta 540
cctgaggcta ttttttcaaa tgtatacact ttctgagatc ccaataaaaa tatgacattt 600
gaatcatgta cctcttatcc tgtctctaag aagctcttgc aagaaatata ttctctgctg 660
tgcttcttag tgttctacat tattccactc tctattatct ctgtctacta ttctctgatt 720
gctaggaccc tttacaaaag caccctgaac atacctactg aggaacaaag ccatgcccgt 780
aagcagattg aatcccgaag gagaattgcc agaacgggtat tgggtgttgg ggctctgttt 840
gccctctgct ggttgccaaa tcacctcctg tacctctacc attcattcac ttctcaaac 900
tatgtagacc cctctgccat gcatttcatt ttcaccattt tctctcgggt tttggctttc 960
agcaattctt gcgtaaaccc ctttgctctc tactggctga gcaaaagctt ccagaagcat 1020
tttaaagctc agttgttctg ttgcaaggcg gagcggcctg agcctcctgt tgctgacacc 1080
tctcttacca cctggctgt gatgggaacg gtcccgggca ctgggagcat acagatgtct 1140
gaaattagtg tgacctcgtt cactgggtgt agtgtgaagc aggcagagga cagattctag 1200

<210> 18
<211> 1200
<212> DNA
<213> Rattus norvegicus

<400> 18
atgtctcaaa ggcagcctca gtcacctaata cagacttta tttccattac aaatgacaca 60
gaaacatcaa gctctgccgt ctccaacgat actacaccta aaggatggac cggagacaac 120
tctccaggaa tagaagcact gtgtgccatc tatatcactt atgctgtgat catttcagtg 180
ggcatcctcg gaaatgctat cctcatcaaa gtctttttca agactaaatc catgcaaaca 240
gttccaaata ttttcatcac cagcctggct tttggagatc tgttactcct gctgacttgt 300
gtgccagtgg atgcaaccca ctacctggca gagggatggc tgtttggaaa ggtcgggtgt 360
aaagtgcctt ctttcatccg gctcacttct gtcgggtgat cagtgttcac gctgacaatt 420
ctcagcgtcg acagatacaa agcagtcgtg aagccacttg aacgacagcc ctccaatgcc 480
attctgaaga cctgtgccaa agctgggtgg atctggatca tggctatgat atttgctctg 540
ccagaggcta tattctcaaa tgtatacact ttccaagatc ctaacagaaa cgtaacattt 600
gaatcctgta actcctaccc tatctctgag aggcttttgc aggaatataa ttctctgttg 660
tgtttcttgg tgttctacat tatcccgctc tcgattatct ctgtctatta ttctttgatt 720
gccaggactc tttacaaaag caccttgaac ataccgactg aggaacaaag ccatgcccga 780
aagcagattg aatcccgaag gagaattgcc aaaacgggtac tgggtgctgg ggctctgttc 840
gcactctgct ggttgccgaa tcacctcctg tatctctatc actcattcac ttatgaaagc 900
tacgcagagc cttctgatgt ccctttcgtt gtcaccattt tctctcgggt gctggctttc 960
agtaattcct gcgtgaaccc ctttgctctg tattggctga gcaagacctt ccagaagcat 1020
tttaaaggctc agctctgctg cttcaaggca gagcagcctg aacctcctct tgggtgacacc 1080
ccccttaaca acctcactgt gatggggcgg gttccagcta ctgggagtg acacgtctct 1140
gaaattagcg tgacctcgtt tagtggcagt actgccaaga aaggagagga caaagttag 1200

<210> 19
<211> 1199
<212> DNA
<213> Artificial Sequence

<220>

<223> BRS-3 consensus sequence

<400> 19

```

atggctcaaa ggcagcctca ctcacctaata cagacttttaa tttcaatcac aaatgacaca 60
gaacatcaag ctctgtgggt tctaacgata acacaaataa aggatggagc ggggacaact 120
ctccaggaat agaagcattg tgtgccatct atattactta tgctgtgata atttcagtgg 180
gcatccttgg aaatgctatt ctcaccaaag tctttttcaa gaccaaatac atgcaaacag 240
ttccaaatat tttcatcacc agcctggctt ttggagatct tttacttctg ctaacttgtg 300
tgccagtgga tgcaaccac taccttgcag aaggatggct gttcggaaga attggttcta 360
aggtgctctc tttcatccgg ctcacttctg ttggtgtgtc agtggtcacg ttaacaatc 420
tcagcgctga cagatacaag gcagttgtga agccacttga gcgacagccc tccaatgcca 480
tcctgaagac ttgtgtaaaa gctggctgcg tctggatcgt gtctatgata tttgctctac 540
ctgaggctat attttcaaat gtatacactt ttcgagatcc caacaaaaat gtgacatttg 600
aatcatgtac ctcttaccct gtctctaaga agctcttgca agaaatacat tctctgctgt 660
gcttcttagt gttctacatt attccactct ctattatctc tgtctattat tctttgattg 720
ctaggaccct ttacaaaagc accctgaaca tacctactga ggaacaaagc catgcccgta 780
agcagattga atcccgaag agaattgcca gaacgggtatt ggtggttggtg gctgtggttg 840
ccctctgctg gttgccaaat cactcctgt acctctacca ttcattcact tctcaaacct 900
atgtagaccc ctctgccatg catttcatct tcaccatttt ctctcgggtt ctggctttca 960
gcaattcttg cgtaaaaccc tttgctctct actggctgag caaaccttc cagaagcatt 1020
ttaaagctca gttgttctgt tgcaaggcag agcagcctga gcctcctgtt gctgacacct 1080
ctcttaccac cctggctgtg atgggaaggg tcccgggcac tgggagcata cagatgtctg 1140
aaattagtgt gacctcgttc actgggtgta gtgtgaagca ggcagaggac agagtctag 1199

```

<210> 20

<211> 399

<212> PRT

<213> Homo Sapiens

<400> 20

```

Met Ala Gln Arg Gln Pro His Ser Pro Asn Gln Thr Leu Ile Ser Ile
1      5      10      15
Thr Asn Asp Thr Glu Ser Ser Ser Ser Val Val Ser Asn Asp Asn Thr
20      25      30
Asn Lys Gly Trp Ser Gly Asp Asn Ser Pro Gly Ile Glu Ala Leu Cys
35      40      45
Ala Ile Tyr Ile Thr Tyr Ala Val Ile Ile Ser Val Gly Ile Leu Gly
50      55      60
Asn Ala Ile Leu Ile Lys Val Phe Phe Lys Thr Lys Ser Met Gln Thr
65      70      75      80
Val Pro Asn Ile Phe Ile Thr Ser Leu Ala Phe Gly Asp Leu Leu Leu
85      90      95
Leu Leu Thr Cys Val Pro Val Asp Ala Thr His Tyr Leu Ala Glu Gly
100      105      110
Trp Leu Phe Gly Arg Ile Gly Cys Lys Val Leu Ser Phe Ile Arg Leu
115      120      125
Thr Ser Val Gly Val Ser Val Phe Thr Leu Thr Ile Leu Ser Ala Asp
130      135      140
Arg Tyr Lys Ala Val Val Lys Pro Leu Glu Arg Gln Pro Ser Asn Ala
145      150      155      160
Ile Leu Lys Thr Cys Val Lys Ala Gly Cys Val Trp Ile Val Ser Met
165      170      175
Ile Phe Ala Leu Pro Glu Ala Ile Phe Ser Asn Val Tyr Thr Phe Arg
180      185      190
Asp Pro Asn Lys Asn Met Thr Phe Glu Ser Cys Thr Ser Tyr Pro Val
195      200      205
Ser Lys Lys Leu Leu Gln Glu Ile His Ser Leu Leu Cys Phe Leu Val
210      215      220
Phe Tyr Ile Ile Pro Leu Ser Ile Ile Ser Val Tyr Tyr Ser Leu Ile
225      230      235      240
Ala Arg Thr Leu Tyr Lys Ser Thr Leu Asn Ile Pro Thr Glu Glu Gln
245      250      255

```

Ser His Ala Arg Lys Gln Ile Glu Ser Arg Lys Arg Ile Ala Arg Thr
 260 265 270
 Val Leu Val Leu Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Asn His
 275 280 285
 Leu Leu Tyr Leu Tyr His Ser Phe Thr Ser Gln Thr Tyr Val Asp Pro
 290 295 300
 Ser Ala Met His Phe Ile Phe Thr Ile Phe Ser Arg Val Leu Ala Phe
 305 310 315 320
 Ser Asn Ser Cys Val Asn Pro Phe Ala Leu Tyr Trp Leu Ser Lys Ser
 325 330 335
 Phe Gln Lys His Phe Lys Ala Gln Leu Phe Cys Cys Lys Ala Glu Arg
 340 345 350
 Pro Glu Pro Pro Val Ala Asp Thr Ser Leu Thr Thr Leu Ala Val Met
 355 360 365
 Gly Thr Val Pro Gly Thr Gly Ser Ile Gln Met Ser Glu Ile Ser Val
 370 375 380
 Thr Ser Phe Thr Gly Cys Ser Val Lys Gln Ala Glu Asp Arg Phe
 385 390 395

<210> 21
 <211> 399
 <212> PRT
 <213> Rattus norvegicus

<400> 21
 Met Ser Gln Arg Gln Pro Gln Ser Pro Asn Gln Thr Leu Ile Ser Ile
 1 5 10 15
 Thr Asn Asp Thr Glu Thr Ser Ser Ser Ala Val Ser Asn Asp Thr Thr
 20 25 30
 Pro Lys Gly Trp Thr Gly Asp Asn Ser Pro Gly Ile Glu Ala Leu Cys
 35 40 45
 Ala Ile Tyr Ile Thr Tyr Ala Val Ile Ile Ser Val Gly Ile Leu Gly
 50 55 60
 Asn Ala Ile Leu Ile Lys Val Phe Phe Lys Thr Lys Ser Met Gln Thr
 65 70 75 80
 Val Pro Asn Ile Phe Ile Thr Ser Leu Ala Phe Gly Asp Leu Leu Leu
 85 90 95
 Leu Leu Thr Cys Val Pro Val Asp Ala Thr His Tyr Leu Ala Glu Gly
 100 105 110
 Trp Leu Phe Gly Lys Val Gly Cys Lys Val Leu Ser Phe Ile Arg Leu
 115 120 125
 Thr Ser Val Gly Val Ser Val Phe Thr Leu Thr Ile Leu Ser Ala Asp
 130 135 140
 Arg Tyr Lys Ala Val Val Lys Pro Leu Glu Arg Gln Pro Ser Asn Ala
 145 150 155 160
 Ile Leu Lys Thr Cys Ala Lys Ala Gly Gly Ile Trp Ile Met Ala Met
 165 170 175
 Ile Phe Ala Leu Pro Glu Ala Ile Phe Ser Asn Val Tyr Thr Phe Gln
 180 185 190
 Asp Pro Asn Arg Asn Val Thr Phe Glu Ser Cys Asn Ser Tyr Pro Ile
 195 200 205
 Ser Glu Arg Leu Leu Gln Glu Ile His Ser Leu Leu Cys Phe Leu Val
 210 215 220
 Phe Tyr Ile Ile Pro Leu Ser Ile Ile Ser Val Tyr Tyr Ser Leu Ile
 225 230 235 240
 Ala Arg Thr Leu Tyr Lys Ser Thr Leu Asn Ile Pro Thr Glu Glu Gln
 245 250 255
 Ser His Ala Arg Lys Gln Ile Glu Ser Arg Lys Arg Ile Ala Lys Thr
 260 265 270
 Val Leu Val Leu Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Asn His
 275 280 285
 Leu Leu Tyr Leu Tyr His Ser Phe Thr Tyr Glu Ser Tyr Ala Glu Pro
 290 295 300

```

Ser Asp Val Pro Phe Val Val Thr Ile Phe Ser Arg Val Leu Ala Phe
305                               310           315           320
Ser Asn Ser Cys Val Asn Pro Phe Ala Leu Tyr Trp Leu Ser Lys Thr
                               325           330           335
Phe Gln Lys His Phe Lys Ala Gln Leu Cys Cys Phe Lys Ala Glu Gln
                               340           345           350
Pro Glu Pro Pro Leu Gly Asp Thr Pro Leu Asn Asn Leu Thr Val Met
                               355           360           365
Gly Arg Val Pro Ala Thr Gly Ser Ala His Val Ser Glu Ile Ser Val
370                               375           380
Thr Leu Phe Ser Gly Ser Thr Ala Lys Lys Gly Glu Asp Lys Val
385                               390           395

```

<210> 22

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> BRS-3 consensus sequence

<400> 22

```

Met Ala Gln Arg Gln Pro His Ser Pro Asn Gln Thr Leu Ile Ser Ile
1      5      10      15
Thr Asn Asp Thr Glu Ser Ser Ser Ser Val Val Ser Asn Asp Asn Thr
20      25      30
Asn Lys Gly Trp Ser Gly Asp Asn Ser Pro Gly Ile Glu Ala Leu Cys
35      40      45
Ala Ile Tyr Ile Thr Tyr Ala Val Ile Ile Ser Val Gly Ile Leu Gly
50      55      60
Asn Ala Ile Leu Ile Lys Val Phe Phe Lys Thr Lys Ser Met Gln Thr
65      70      75      80
Val Pro Asn Ile Phe Ile Thr Ser Leu Ala Phe Gly Asp Leu Leu Leu
85      90      95
Leu Leu Thr Cys Val Pro Val Asp Ala Thr His Tyr Leu Ala Glu Gly
100     105     110
Trp Leu Phe Gly Arg Ile Gly Cys Lys Val Leu Ser Phe Ile Arg Leu
115     120     125
Thr Ser Val Gly Val Ser Val Phe Thr Leu Thr Ile Leu Ser Ala Asp
130     135     140
Arg Tyr Lys Ala Val Val Lys Pro Leu Glu Arg Gln Pro Ser Asn Ala
145     150     155     160
Ile Leu Lys Thr Cys Ile Lys Ala Gly Cys Val Trp Ile Val Ser Met
165     170     175
Ile Phe Ala Leu Pro Glu Ala Ile Phe Ser Asn Val Tyr Thr Phe Arg
180     185     190
Asp Pro Asn Lys Asn Val Thr Phe Glu Ser Cys Thr Ser Tyr Pro Val
195     200     205
Ser Lys Lys Leu Leu Gln Glu Ile His Ser Leu Leu Cys Phe Leu Val
210     215     220
Phe Tyr Ile Ile Pro Leu Ser Ile Ile Ser Val Tyr Tyr Ser Leu Ile
225     230     235     240
Ala Arg Thr Leu Tyr Lys Ser Thr Leu Asn Ile Pro Thr Glu Glu Gln
245     250     255
Ser His Ala Arg Lys Gln Ile Glu Ser Arg Lys Arg Ile Ala Arg Thr
260     265     270
Val Leu Val Leu Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Asn His
275     280     285
Leu Leu Tyr Leu Tyr His Ser Phe Thr Ser Gln Thr Tyr Val Asp Pro
290     295     300
Ser Ala Met His Phe Ile Phe Thr Ile Phe Ser Arg Val Leu Ala Phe
305     310     315     320
Ser Asn Ser Cys Val Asn Pro Phe Ala Leu Tyr Trp Leu Ser Lys Thr

```


Phe	Gln	Lys	His	325	Phe	Lys	Ala	Gln	Leu	330	Phe	Cys	Cys	Lys	Ala	335	Glu	Gln
			340							345						350		
Pro	Glu	Pro	Pro	Val	Ala	Asp	Thr	Ser	Leu	Thr	Thr	Leu	Ala	Val	Met			
		355					360											
Gly	Arg	Val	Pro	Gly	Thr	Gly	Ser	Ile	Gln	Met	Ser	Glu	Ile	Ser	Val			
	370					375						380						
Thr	Ser	Phe	Ser	Gly	Cys	Ser	Val	Lys	Gln	Ala	Glu	Asp	Arg	Val				
385					390					395								